What is claimed is:

1. A method to determine gender of a canine subject, comprising contacting a nucleic acid sample from the canine subject with at least one probe or primer specific for a canine amelogenin gene, and using the binding of the at least one probe or primer to detect a difference between the canine amelogenin gene on the Y chromosome and the canine amelogenin gene on the X chromosome, thereby determining gender of the canine subject.

2. The method of claim 1, wherein gender of the canine subject is determined by contacting the nucleic acid sample with at least one probe or primer that specifically binds SEQ ID NO:22 and/or SEQ ID NO:23.

3. The method of claim 1, wherein gender of the canine subject is determined by contacting the nucleic acid sample with at least one probe or primer that specifically binds SEQ ID NO:10 and/or SEQ ID NO:11.

4. The method of claim 3, wherein gender of the canine subject is determined by contacting the nucleic acid sample with a primer pair, wherein a first primer of the primer pair specifically binds to SEQ ID NO:6 and/or SEQ ID NO:7 and a second primer of the primer pair specifically binds to SEQ ID NO:8 and/or SEQ ID NO:9.

5. The method of claim 4, wherein the first primer comprises at least 10 nucleotides of SEQ ID NO:3 and the second primer comprises at least 10 nucleotides of SEQ ID NO:5.

6. The method of claim 5, wherein the first primer is SEQ ID NO:3 and the second primer is SEQ ID NO:5.

7. The method of claim 5, wherein the first primer is SEQ ID NO:4 and the second primer is SEQ ID NO:5.

8. The method of claim 5, wherein the primer pair generates an amplification product that is a different length for the amelogenin gene on the X chromosome and the amelogenin gene on the Y chromosome.

9. A method to determine gender of a canine subject, comprising contacting a nucleic acid sample from the canine subject with at least one probe or primer specific for canine amelogenin, and detecting binding of the at least one probe or primer, thereby determining gender of the canine subject.

10. The method of claim 9, wherein gender of the canine subject is determined by contacting the nucleic acid sample with at least one probe or primer that specifically binds SEQ ID NO:22 and/or SEQ ID NO:23.

11. The method of claim 9, wherein gender of the canine subject is determined by contacting the nucleic acid sample with at least one probe or primer that specifically binds SEQ ID NO:10 and/or SEQ ID NO:11.

12. The method of claim 11, wherein gender of the canine subject is determined by contacting the nucleic acid sample with a primer pair, wherein a first primer of the primer pair specifically binds to SEQ ID NO:6 and/or SEQ ID NO:7 and a second primer of the primer pair specifically binds to SEQ ID NO:8 and/or SEQ ID NO:9.

13. The method of claim 9, wherein binding of the at least one probe or primer distinguishes the canine amelogenin gene on the X chromosome from the amelogenin gene on the Y chromosome.

14. A method to determine gender of a canine subject, comprising contacting a nucleic acid sample from the canine subject with at least one probe or primer specific for canine amelogenin, and detecting binding of the at least one probe or primer to a target region of the canine amelogenin gene and/or detecting an extension product of the canine

amelogenin gene generated from the at least one primer, wherein a difference in the binding of the at least one probe or primer, or a difference in the extension product generated using the at least one primer distinguishes a copy of the canine amelogenin gene on the X chromosome from a copy of the canine amelogenin gene on the Y chromosome, thereby determining gender of the canine subject.

15. The method of claim 14, wherein the target region is within 500 nucleotides of a nucleotide position that is different between the amelogenin gene on the X chromosome and the amelogenin gene on the Y chromosome.

16. The method of claim 14, wherein gender of the canine subject is determined by contacting the nucleic acid sample with at least one probe or primer that specifically binds SEQ ID NO:22 and/or SEQ ID NO:23.

17. The method of claim 14, wherein gender of the canine subject is determined by contacting the nucleic acid sample with at least one probe or primer that specifically binds SEQ ID NO:10 and/or SEQ ID NO:11.

18. The method of claim 17, wherein gender of the canine subject is determined by contacting the nucleic acid sample with a primer pair, wherein a first primer of the primer pair specifically binds to SEQ ID NO:6 and/or SEQ ID NO:7 and a second primer of the primer pair specifically binds to SEQ ID NO:8 and/or SEQ ID NO:9.

19. A method to determine gender of a canine subject, comprising contacting a nucleic acid sample from the canine subject with at least one probe or primer specific for canine amelogenin, and detecting a canine amelogenin gene on the Y chromosome based on binding of the probe or primer, thereby determining gender of the canine subject.

20. The method of claim 19, wherein gender of the canine subject is determined by contacting the nucleic acid sample with at least one probe or primer that specifically binds SEQ ID NO:22 and/or SEQ ID NO:23.

21. The method of claim 19, wherein gender of the canine subject is determined by contacting the nucleic acid sample with at least one probe or primer that specifically binds SEQ ID NO:10 and/or SEQ ID NO:11.

22. The method of claim 21, wherein gender of the canine subject is determined by contacting the nucleic acid sample with a primer pair, wherein a first primer of the primer pair specifically binds to SEQ ID NO:6 and/or SEQ ID NO:7 and a second primer of the primer pair specifically binds to SEQ ID NO:8 and/or SEQ ID NO:9.

23. A method to detect binding of at least one primer or probe to a canine amelogenin gene, comprising contacting a nucleic acid sample from a canine subject with at least one probe or primer specific for canine amelogenin.

24. The method of claim 23, wherein the nucleic acid sample is contacted with at least one probe or primer that specifically binds SEQ ID NO:22 and/or SEQ ID NO:23.

25. The method of claim 23, wherein the nucleic acid sample is contacted with at least one probe or primer that specifically binds SEQ ID NO:10 and/or SEQ ID NO:11.

26. The method of claim 25, wherein the nucleic acid sample is contacted with a primer pair, wherein a first primer of the primer pair specifically binds to SEQ ID NO:6 and/or SEQ ID NO:7 and a second primer of the primer pair specifically binds to SEQ ID NO:8 and/or SEQ ID NO:9.

27. The method of claim 26, wherein the first primer comprises at least 10 nucleotides of SEQ ID NO:3 and the second primer comprises at least 10 nucleotides of SEQ ID NO:5.

28. The method of claim 26, wherein the first primer is SEQ ID NO:3 and the second primer is SEQ ID NO:5.

29. The method of claim 26, wherein the first primer is SEQ ID NO:4 and the second primer is SEQ ID NO:5.

30. The method of claim 26, wherein the primer pair generates an amplification product that is a different length for the X and Y chromosome.

31. The method of claim 23, further comprising detecting binding of another at least one probe or primer to a canine microsatellite locus.

32. The method of claim 31, wherein the microsatellite locus is at least one of PEZ1/CATA1, PEZ3, PEZ5, PEZ6, PEZ8, PEZ10, PEZ11, PEZ12, PEZ13, PEZ15, PEZ16, PEZ17, PEZ20, PEZ21, FH2010 (Fred Hutchinson marker 2010), FH2054, and FH2079.

33. The method of claim 32, wherein binding of at least one primer or probe to PEZ1/CATA1, PEZ3, PEZ5, PEZ6, PEZ8, PEZ12, PEZ20, FH2010, FH2054, and FH2079 is detected.

34. The method of claim 32, wherein binding of at least one primer or probe to PEZ10, PEZ11, PEZ13, PEZ15, PEZ16, PEZ17, and PEZ21 is detected.

35. The method of claim 32, wherein binding of at least one primer or probe to PEZ1/CATA1, PEZ3, PEZ5, PEZ6, PEZ8, PEZ12, PEZ16, PEZ17, PEZ20, PEZ21, FH2010, FH2054, and FH2079 is detected.

36. A method to genotype a canine subject, comprising contacting a nucleic acid sample from the canine subject with at least one probe or primer specific for canine amelogenin, and detecting binding of the at least one probe or primer, thereby genotyping the canine subject.

37. The method of claim 36, wherein the nucleic acid sample is contacted with at least one probe or primer that specifically binds SEQ ID NO:22 and/or SEQ ID NO:23.

38. The method of claim 36, wherein the nucleic acid sample is contacted with at least one probe or primer that specifically binds SEQ ID NO:10 and/or SEQ ID NO:11.

39. The method of claim 38, wherein the nucleic acid sample is contacted with a primer pair, wherein a first primer of the primer pair specifically binds to SEQ ID NO:6 and/or SEQ ID NO:7 and a second primer of the primer pair specifically binds to SEQ ID NO:8 and/or SEQ ID NO:9.

40. The method of claim 39, wherein the first primer comprises at least 10 nucleotides of SEQ ID NO:3 and the second primer comprises at least 10 nucleotides of SEQ ID NO:5.

41. The method of claim 39, wherein the first primer comprises at least 15 nucleotides of SEQ ID NO:3 and the second primer comprises at least 10 nucleotides of SEQ ID NO:5.

42. The method of claim 41, wherein the first primer is SEQ ID NO:3 and the second primer is SEQ ID NO:5.

43. The method of claim 41, wherein the first primer is SEQ ID NO:4 and the second primer is SEQ ID NO:5.

44. The method of claim 36, further comprising genotyping the canine subject at a microsatellite locus.

45. The method of claim 44, wherein the microsatellite locus comprises a repeated tetranucleotide motif consisting of AAA or TTT, with the fourth residue of the tetranucleotide repeat motif being any one of G, C, A or T.

46. The method of claim 44, wherein a panel of at least 5 microsatellite loci are genotyped.

47. The method of claim 44, wherein the microsatellite locus comprises a repeated motif selected from AAAG, GAAA, AAAT, TTTC, CTTT, TTTA, AAGG, GAAT, GAAG, GAAAA, AAAAAG, TGC and TTC.

48. The method of claim 44, wherein the microsatellite locus is at least one of PEZ1/CATA1, PEZ3, PEZ5, PEZ6, PEZ8, PEZ10, PEZ11, PEZ12, PEZ13, PEZ15, PEZ16, PEZ17, PEZ20, PEZ21, FH2010, FH2054, and FH2079.

49. The method of claim 44, wherein the microsatellite loci PEZ1/CATA1, PEZ3, PEZ5, PEZ6, PEZ8, PEZ12, PEZ20, FH2010, FH2054, and FH2079 are genotyped.

50. The method of claim 44, wherein the microsatellite loci PEZ10, PEZ11, PEZ13, PEZ15, PEZ16, PEZ17, and PEZ21 are genotyped.

51 The method of claim 44, wherein the microsatellite loci PEZ1/CATA1, PEZ3, PEZ5, PEZ6, PEZ8, PEZ12, PEZ16, PEZ17, PEZ20, PEZ21, FH2010, FH2054, and FH2079, are genotyped.

52. The method of claim 44, wherein the genotyping provides for the determination of both gender and identity of the canine subject.

53. The method of claim 44, wherein the genotyping further provides for a determination of parentage of the canine subject.

54. An oligonucleotide that specifically binds to SEQ ID NO:10 and/or SEQ ID NO:11, wherein the oligonucleotide is between 10 and 50 nucleotides in length.

55. The oligonucleotide of claim 54, wherein the oligonucleotide comprises at least 10 contiguous nucleotides of at least one of SEQ ID NOS:1 to 5.

56. The oligonucleotide of claim 55, wherein the oligonucleotide comprises at least 15 contiguous nucleotides of any one of SEQ ID NOS:1 to 5.

57. The oligonucleotide of claim 54, wherein the oligonucleotide is at least 15 nucleotides in length.

58. The oligonucleotide of claim 54, wherein the oligonucleotide is any one of SEQ ID NOS:1 to 5.

59. The oligonucleotide of claim 54, wherein the oligonucleotide comprises a detectable label.

60. A primer pair, wherein one primer of the primer pair specifically binds to SEQ ID NO:6 and/or SEQ ID NO:7, and one primer of the primer pair specifically binds to SEQ ID NO:8 and/or SEQ ID NO:9, wherein the a first primer of the primer pair and a second primer of the primer pair are at least 10 nucleotides in length.

61. The method of claim 60, wherein the first primer comprises at least 10 nucleotides of SEQ ID NO:3 and the second primer comprises at least 10 nucleotides of SEQ ID NO:5.

62. The method of claim 61, wherein the first primer is SEQ ID NO:3 and the second primer is SEQ ID NO:5.

63. The method of claim 61, wherein the first primer is SEQ ID NO:4 and the second primer is SEQ ID NO:5.

64. The method of claim 61, wherein the primer pair generates an amplification product that is a different length for the X and Y chromosome.

65. An isolated polynucleotide comprising at least 100 contiguous nucleotides of SEQ ID NOS:22 or 23, or a complement thereof.

66. The isolated polynucleotide of claim 65, wherein the polynucleotide comprises at least 400 contiguous nucleotides of SEQ ID NOS:22 or 23, or a complement thereof.

67. The isolated polynucleotide of claim 65, wherein the polynucleotide comprises SEQ ID NO:22, or a complement thereof.

68. The isolated polynucleotide of claim 65, wherein the polynucleotide comprises SEQ ID NO:23, or a complement thereof.

69. A vector comprising the isolated polynucleotide of claim 65.

70. An isolated cell comprising the vector of claim 69.

71. An isolated polypeptide encoded by SEQ ID NO:22.

72. An isolated polypeptide encoded by SEQ ID NO:23.

73. An isolated polynucleotide that encodes the polypeptide encoded by SEQ ID NOS:22 or 23, or a complement thereof.

74. A method for quality control testing of a nucleic acid sample from a canine subject, comprising determining gender of the canine subject using a gender marker, and comparing the determined gender with a known gender of the canine subject.

75. The method of claim 74, further comprising genotyping at least one microsatellite locus.

76. The method of claim 74, wherein the quality control testing and the genotyping are performed in the same reaction.

77. The method of claim 76, wherein the reaction is an amplification reaction.